

【SEQUENCE LISTING】

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel phytochrome-interacting protein and a use thereof

<130> OP05-1002

<150> KR 10-2004-0013663
<151> 2004-02-27

<160> 15

<170> KopatentIn 1.71

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<212> DNA
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<220>
<223> PCR primer

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ggatccaaat gtcaggctct aggccgact 29

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ctcgagctac ttgttgctg cagcgagttc 30

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<213> Arabidopsis thaliana

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gaactcaaca gcaacaacgc tgtgtattgg gcaaatcgtg catttgctca cacaaaactg	180
gaggaatatg gcagtgaat acaggatgca tcgaaggcca tgaagtga ttcaagatac	240
tctaagggtt attacaggcg tgggtgctcg tatcttgcca tgggaaaatt taaggatgcc	300
ttgaaggact tccaacaggt aaaaaggctt tctcctaag accctgatgc cacaagaaag	360
ctaaaggaat gtgagaaagc agtgatgaaa ctcaaattg aagaagcaat ctctgtgcca	420
gtatctgaaa ggcgttcagt agctgagtc attgactcc atacaataga ggttgagcca	480
caatatctg gtgctagaat tgaggagag gaagttacct tagattttgt gaaaacgatg	540
atggaggatt ttaagaacca aaaaacattg cataaacggt atgcctatca aatcgtctta	600
cagactaggc aaatcttgct agcactgcct tctctgttg atataagtgt tccacatggc	660
aaacatatca ctgtttcggg tgacgttcat ggtcagtct acgatcttct caatatcttt	720
gagcttaatg gcctccctc ggaggagaac ccatacctat ttaatggcga ctttgggac	780
agaggctcat tctccgttga gatcctcct accttgttg ctttcaagt catgtgccca	840
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atgggtaata agggagcctt cattcgtttt gaagctcctg atatgaagcc aaacattgtt	1380

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aggatgttca actaa 1455

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 <212> PRT
 <213> Arabidopsis thaliana

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Lys Ser Gln Ala Asn Glu Ala Phe Lys Gly His Lys Tyr Ser Ser Ala
 20 25 30

Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
 35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
 50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
 65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
 85 90 95

Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro
 100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
 115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
 130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
 145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
 165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
 180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
 195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
 210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
 225 230 235 240

Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
 245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
 260 265 270

Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
 275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
 290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
 305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
 325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
 340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
 355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
 370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
 385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
 405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
 420 425 430

Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
 435 440 445

Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
 450 455 460

Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
 465 470 475 480

Arg Met Phe Asn

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 ggatccatgg agaccaagaa tgag 24

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<400> 6
 ctcgagttag ttgaacatcc tgag 24

<210> 7
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<400> 7

ggatccgatg tcaggctcta ggccgact

28

<210> 8

<211> 34

<212> DNA

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<223> PCR primer

<400> 8

gctgatcagc atggttccg ggtcggggg tagt

34

<210> 9

<211> 34

<212> DNA

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<223> PCR primer

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cccggccgga ctaatatggc atcatcagca tcac

34

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<212> DNA

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<223> PCR primer

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ctcgagtcaa gagattgctt ctcaaaa

27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 11

ggatccatgc cagtatctga aaggcgt

27

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12

atggagacca agaatgagaa ttct

24

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 13

ttagttgaac atcctgagaa agtt

24

<210> 14

<211> 347

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Ser Val Pro Val Ser Glu Arg Arg Ser Val Ala Glu Ser Ile Asp Phe

1

5

10

15

His Thr Ile Glu Val Glu Pro Gln Tyr Ser Gly Ala Arg Ile Glu Gly

20

25

30

Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys

35

40

45

Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
 50 55 60
 Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
 65 70 75 80
 Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe
 85 90 95
 Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu
 100 105 110
 Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
 115 120 125
 Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser
 130 135 140
 Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys
 145 150 155 160
 Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe
 165 170 175
 Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val
 180 185 190
 Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp
 195 200 205
 Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro
 210 215 220
 Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro
 225 230 235 240
 Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly
 245 250 255
 Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu
 260 265 270
 Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp
 275 280 285
 Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met

290	295	300	
Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro			
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Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn			
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 acgatgatgg aggattttaa gaacaaaaa acattgcata aacggtatgc ctatcaaac 180
 gtcttacaga ctaggcaaat ctgctagca ctgccttctc ttgttgatat aagtgtcca 240
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 atctttgagc itaatggcct cccttcggag gagaacccat acctatttaa tggcgacttt 360
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 tatggttttg agggtagagt tcggtccaag ttgagtgaag aattcgtgga tctcttgct 540
 gaagttttct gttacctccc gttggctcat gttataaatg ggaaggctct cgtggtacat 600
 ggaggtcttt tcagtgtga cggcgtgaaa ctctcagaca tcagagccat tgacagattc 660
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gatcagatgg gtaataaggg agccttcatt cgtttgaag ctctgatat gaagccaaac 960

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tttctcagga tgttcaacta a 1041